Amendments to the Claims

This listing of claims will replace all prior versions and listings of claims in the application:

Claims 1-11 (cancelled)

12. (Previously presented) A method for generating a secondary library of protein variants of a target protein comprising:

a) inputting the coordinates of said target protein into a computer;
b) utilizing a forcefield calculation to generate a primary library comprising a plurality of primary variant amino acid residues at primary variant positions;
c) computationally generating a probability distribution table of variant amino acid residues in a plurality of said primary variant positions; and
d) combining a plurality of said primary variant amino acid residues to generate a secondary library of secondary variant proteins.

13. (Previously presented) A method according to claim 12, wherein said force field calculation is Self-Consistent Mean Field (SCMF).

Claims 14-20 (Cancelled)

21. (Previously presented) A method according to claim 12 wherein said combining comprises:
a) generating a set of oligonucleotide probes each encoding at least one of said primary variant amino acid residues;
b) using said probes in a polymerase chain reaction (PCR) to generate a plurality of oligonucleotide sequences, each encoding said secondary variant sequences; and
c) producing said secondary variant sequences in host cells transformed with said oligonucleotide sequences.

22. (Previously presented) A method according to claim 21 wherein said PCR is multiple PCR wherein said probes are pooled.

23. (Previously presented) A method according to 22 wherein said probes are added in equimolar amounts.

24. (Previously presented) A method according to claim 23 wherein said probes are combined in amounts that correspond to the frequency of the said variant amino acid residues in said probability distribution table.

Claims 25-32 (cancelled)